

Untitled-12 Formatted Alignment

HTLV-I/II: GIV-I  
Env Alignment

HTLV-II Env	M-----	GIVF	--FLI-----	LFS-----	11			
HTLV-I Env	M-----	GKFL	ATLIL-----	FFQ-----	13			
HIV SF2 Env	M-----	MTARGTRKNY	QRLWRWGTML	LGMLMICSAA	ENLWVTVYYG	VPVWKEATT	50	
Consensus	M-----	Q...L	...L-----	.F.-----	50			
HTLV-II Env	-LT---	HFPPL	AQ--QS-----	R-----	TLTIC	IS	SY-----	32
HTLV-I Env	-FC---	PLIF	GDYSPS-----	C-----	TLTIC	VS	SY-----	36
HIV SF2 Env	LFCASDARAY	ATEVHNWAT	HACVPTDPNP	QEVLICNVTE	NFDMWKNNMV	100		
Consensus	-FC-----	....A....S-----	.....C-----	TLTIC	..S	SY-----	100	
HTLV-II Env	-----	HS	SPGSP	TQEVG-----	-----	I-----	-----	45
HTLV-I Env	-----	IS	KPONP	AQPVC-----	-----	C-----	-----	49
HIV SF2 Env	EQMQEDEIISL	WDQSLKPGVK	LTPLCVTLDC	TDVNNTTSSSL	RNATNTTSSS	150		
Consensus	-----	IS	KPQ.P	QEMV-----	-----	S-----	-----	150
HTLV-II Env	M-----	-----	-----	N-----	LNSLT	TDO-----	R-----	60
HTLV-I Env	M-----	-----	-----	-----	LLALS	ADG-----	AD-----	64
HIV SF2 Env	NETMEKGELK	NCSFNTTTSI	RDKMQEQQYAL	FYKIDVLPID	KNDTKFRRI	200		
Consensus	-----	-----	-----	LL.L.	DQ-----	R-----	H-----	200
HTLV-II Env	-----	PFC	PNL-----	I-----	SGF-----	HKTY-----	-----	77
HTLV-I Env	-----	PFC	PNL-----	V-----	SSY-----	HATYS-----	-----	81
HIV SF2 Env	CNTSTITQAC	PKISFEPIM	HYCTPAGFAI	LKCNDKKFNG	TGPCTNVSTV	250		
Consensus	-----	PFC	PNL-----	.Y-----	SGF-----	HKTY-----	-----	250
HTLV-II Env	-----	-----	-----	-----	-----	-----	-----	81
HTLV-I Env	-----	-----	-----	-----	-----	-----	-----	85
HIV SF2 Env	QCTHGIKPVV	STQNLNGSL	AAAAEVIIRSS	N-----	NNNAKIII	VQLNKSVEIN	300	
Consensus	-----	-----	-----	-----	-----	-----	-----	300
HTLV-II Env	-----	-----	-----	-----	-----	WIK-----	-----	86
HTLV-I Env	-----	-----	-----	-----	-----	WIK-----	-----	90
HIV SF2 Env	CTR	PNTRN	RISIGPGRF	HTTKQIIGDI	RQAHCNLSRA	TWEITLEQIA	350	
Consensus	-----	-----	-----	-----	-----	WIK-----	-----	350
HTLV-II Env	-----	KPNP	GLGYYS	SYN-----	S-----	LQEP-----	Y-----	110
HTLV-I Env	-----	KPNP	GGGYYS	SY-----	S-----	LQEP-----	Y-----	114
HIV SF2 Env	TKLRKQFRNK	TIAFDRSSGG	PEIVMHSFN	CGGEFFY	GNT	SQLFNSTWND	400	
Consensus	-----	KPNP	G.GYYS	SY-----	S-----	LQEP-----	Y-----	400
HTLV-II Env	-----	-----	-----	-----	TS	AMIGPVSS-----	-----	126
HTLV-I Env	-----	-----	-----	-----	TC	EMIGAVSS-----	-----	130
HIV SF2 Env	TTRANSTEVT	ITIEERIKQI	VIMPQEVGKA	MYAPPISGQI	RCSSKITGLL	450		
Consensus	-----	-----	-----	-----	T.	MIIGPVSS-----	-----	450

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HTLV-II Env	-----	S	F	-----	131				
HTLV-I Env	-----	Y	F	-----	135				
HIV SF2 Env	LTRDGGKNTT	NGIEIFRPG	GDMRDNRSE	LYKKVVKIE	PLGVAPTKAR	500			
Consensus	-----	I	F	-----	500				
HTLV-II Env	-----	HSD	VN	-----	137				
HTLV-I Env	-----	OHD	VN	-----	141				
HIV SF2 Env	RRVVOREKRA	VGMLGAMFLG	LGAAGSTMG	ARSMTLTQVA	RQLLSGIVQQ	550			
Consensus	-----	Q.D	VN	-----	550				
HTLV-II Env	-----	T Q	VSQVSLRL	HFSK	CGSS	156			
HTLV-I Env	-----	T Q	VSRLNINL	HFSK	CGFP	160			
HIV SF2 Env	QNNLLRAIEA	CHLLQLTVW	GHKQLQARVL	AVERYLKDQQ	LLGIWGSGK	600			
Consensus	-----	T Q	VSQVSLRL	HFSK	CG..	600			
HTLV-II Env	M-----	-----	-----	-----	YMIA	163			
HTLV-I Env	F-----	-----	-----	-----	YMIA	167			
HIV SF2 Env	LICTTTPVPWN	ASWSNKIDE	IWDNMTIWMQW	EREIDNYTHL	IYDNEESQN	650			
Consensus	-----	C	-----	-----	YMIA	650			
HTLV-II Env	-----	H	-YDP---I	MF ITSEPTQPPP	TSPPLVHDSD	191			
HTLV-I Env	-----	H	-YDP---I	MF LNTEPSQLPP	TAPPLLPHSN	195			
HIV SF2 Env	QQEKNEQELL	ELDKWAQCLWS	WFSITNWLY	I-----	-----	681			
Consensus	-----	H	-YDP---I	MF I..EP.Q.PP T.PPL...S.	700				
HTLV-II Env	LEHVLTSTS	WTTKILKF	Q	LTLQSTNYSC	MVCDRSSS	SWHLYPNI	241		
HTLV-I Env	LDHILEPSIP	WKSLLT	Q	LTLQSTNYTC	IVCDRAS	TWHLYSPNV	245		
HIV SF2 Env	-----	-----	-----	I-----	GGIV GLRIVF	EV-L	701		
Consensus	L.H.L.PS..	W..KIL.F	Q	LTLQSTNY.C	IACDR.S	SWHLYPNI.	750		
HTLV-II Env	SIPOQTS	SRT	ILFPS	ALPA PP-SQFPWT	HCY PRLQAI	TTDNCNNNSII	290		
HTLV-I Env	SIP-SSS	STP	LLYPS	ALPA PHLTLPFNWT	HCF PQIQAI	VSSPCHNSLI	294		
HIV SF2 Env	SI	---VNVRV	QGYSP	-----	-----	FTR-----	719		
Consensus	SI	..SS..	.LYPS	ALPA P.-..PF.WT	HCF QPR.QAI	....C.NS.I	800		
HTLV-II Env	PFSLAPVP	PPATRRF	AV	PIAVWLVSAL	AA	TGIAGG	TGSLSLASSK	340	
HTLV-I Env	PFSLSPVP	TLGSRSP	AV	PVAVWLVSAL	AM	AGVAGG	TGMSMSLASGK	344	
HIV SF2 Env	-----	-----	-----	-----	-----	PDRPEG	EEE-----	735	
Consensus	PFSL.PVP	....R.R	AV	P.AVWLVSAL	A.G.G.AG	-----	TGS.SLAS.K	850	
HTLV-II Env	SLLLEV	KII	SHLTQAIKV	NHQNII	PRMAQY	AAQNRRG	DL	TFWCGGCK	390
HTLV-I Env	SLLHEV	KII	SQLTQAIKV	NHKNI	KAQY	AAQNRRG	DL	TFWCGGCK	394
HIV SF2 Env	-----	GGF	-----	RDRSGRF	MDGF	-----	-----	R	760
Consensus	SLL.EV	KII	S.LTQAIKV	N.H.N.	MAQY	AAQNRRG	DL	TFWCGGCK	900

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HTLV-II Env	[REDACTED]	IHQEQCCFLN ISNTHVSMLQ ERPHLEKRVVI TGWGLNWDTG	[REDACTED] DSQWREALQ	440
HTLV-I Env	[REDACTED]	ALQEQCQCRFPN ITNSHVPMLQ ERPHLEENRVL TGWGLNWDTG	[REDACTED] DSQWREALQ	444
HIV SF2 Env	[REDACTED]	SL-CLFSYHR LRDLILIMAR IVELEGRGRGW EVLKYWWTI-	[REDACTED] GQYWSQELKN	808
Consensus	[REDACTED]	ALQEQC.F.NP I.N.HV.SLQ ERPHLE.EV. TGWGLNWDTG	[REDACTED] DSQWREALQ	950
HTLV-II Env	[REDACTED]	AGTIIILALLL LVVILGPCIL RQIQALPDR- LQNRRHNQYSL INPEITML	[REDACTED]	486
HTLV-I Env	[REDACTED]	AGTIIILVALLL LVVILAGPCIL RQLRHLPSR- VRYPHYSL-- IKPESSL	[REDACTED]	488
HIV SF2 Env	[REDACTED]	SVISLLNATA IAVAEQTDRV IETVQRAYRA FLNIPRRIRQ GLERAIL	[REDACTED]	855
Consensus	[REDACTED]	AGTIIILALLL LVVIL.GPCIL RQI..LP.R- ..N.H..... I.PE..	[REDACTED]	997

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HTLV-I(II) Env  
Alignment

HTLV-II Env	MGNVF--FILSLSLTHFPLA Q--CSRCGELTIGIISSVHSSPCEPIOPVCF	46
HTLV-I Env	MGKFLATLILPQQFCPLIFG DYSPSCGELTIGIISSVHSSPCEPIOPVCF	50
Consensus	MG.....I.....S.....T.....SSVHS.....C.....Q.....	50
HTLV-II Env	NEDDINSITIDCGIICPPCPNLITYSGFEKITYSLYLEPHMVKKPNRQCGGY	96
HTLV-I Env	IDLADPSADQPPCPNLMSYSSYHATYSLYLEPHMVKKPNRNGGGY	100
Consensus	IDL.....DQ.....PPCPNL.....VS.....HATYSLYLEPHMVKKPNRQCGGY	100
HTLV-II Env	SFSYNDPGSTCPVIGCCSNWTSAYTGEVSSPSWKEHSDVNFTQEVSOVL	146
HTLV-I Env	SASYSNDPGSTKCPVIGCCSNWTCPYTCAVSSPMWKEQHDVNFTQEVSRLN	150
Consensus	S.....SYNDPGSTCPVIGCCSNW.....VSS.....E.....WKE.....DN.....EV.....	150
HTLV-II Env	RHHFSKGCGSSMTIHLVDAPGYDPINWLTSEPTDOPPTIHPPIVHDSDVH	196
HTLV-I Env	NLHFSKGCGFPFSIHLVDAPGYDPINWLTSEPTDOPPTIHPPILPHSNLPH	200
Consensus	.....HFSKGCG.....IHLVDAPGY.....DOPPTIHPPI.....S.....N.....	200
HTLV-II Env	TTESTSWIKILKPKILOLTIOSITVNSCMVQMDRASESSSWHVIYIDNTISIPOQ	246
HTLV-I Env	EPSTIRAKSKLITLALOITIOSITVNSCMVQMDRASESSSWHVIYSPNMSVP-S	249
Consensus	ES.....K.....K.....I.....I.....S.....V.....S.....V.....P.....	250
HTLV-II Env	TSSRTIIFPSLALPAPP-SQPFPTWCHYQPRLQATITDNCNNSTIIPPR	295
HTLV-I Env	SSSTPLIYPSLALPAPHLTLIPFWTHGFLPQIQATIVSSPCNNSTIIPPR	299
Consensus	SS.....I.....I.....I.....I.....P.....Q.....I.....P.....I.....	300
HTLV-II Env	FDFMPPPATIRRRAVPIIAWWLVSALAMCIGIAGGVMGSSTDASSKSNSD	345
HTLV-I Env	IISPVITLGSRIRRRAVPIIAWWLVSALAMCIGIAGGVMGSSTDASSKSNSD	349
Consensus	.....F.....P.....I.....I.....W.....A.....S.....S.....S.....	350
HTLV-II Env	VDKDIDS-TIGAVKHNKNDIIRMAOYAAONRIGDIBBNSVDOCEYCKA	395
HTLV-I Env	VDKDIDS-TIGAVKHNKNDIIRMAOYAAONRIGDIBBNSVDOCEYCKA	399
Consensus	.....V.....D.....I.....I.....I.....I.....I.....I.....	400
HTLV-II Env	GCELVNSIHEVSYIOPRPLSKRYVLTGCLNADIGLSONARBLAQIENHI	445
HTLV-I Env	GRRERNINSHVPRVIOPRPLENRVLIGCLNADIGLSONARBLAQIENHI	449
Consensus	.....G.....E.....I.....I.....I.....I.....I.....I.....	450
HTLV-II Env	LAHLLRNWIFGPQELRQIQAEPQLQNRANQYSLINPSIM	486
HTLV-I Env	VALHLLRNWIFGPQELRQIQAEPQLQNRANQYSLINPSIM	488
Consensus	.....A.....I.....I.....I.....I.....I.....I.....I.....	491

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# HIV-II R1 Alignment

HTLV-II Pol	HRSRPYGYTP DTRARAGKAP RHPDPRRWA	NQHPVQTTPN PPTHILALPK	50
HTLV-I Pol	GKKAACNL-	-NTGASRPAWA	PK
Consensus	.....	...PWA	PK
HTLV-II Pol	VPRYPFLLPL RHPQQMDHHW KGRPTTMPGA SIPPRRPQPP PIAANSHSKH		100
HTLV-I Pol	APR		26
Consensus	...PR		100
HTLV-II Pol	HRPRTPSPTS PSQPISEPKPE RIQAI NDIVS	KALEAGHTIEP YSGPGNNPVE	150
HTLV-I Pol	----- NQFVPEKPE RIQAI QHLVR	KALEAGHTIEP YIGPGNNPVE	65
Consensus	.... PPKPE RIQAV ..AV	KALEAGHTIEP YIGPGNNPVE	150
HTLV-II Pol	EVKKIENCKMR FIDHDERAVNA IIPPIIISGSPSP GPPDDEIISPII ATEPHQDDE		200
HTLV-I Pol	EVKKIANGCKMR FIDHDERAVNS IIAIDSSSSSP GPPDDEIISPII ATEPHQDDE		115
Consensus	EVKKI ENCKMR FIDHDERAVNA IIPPIIISGSPSP GPPDDEIISPII ATEPHQDDE		200
HTLV-II Pol	TDAFFPQIPDP KQMYVPAISI UPSCCNVGPQ TRVAIIIVLPO GEKNSPHARE		250
HTLV-I Pol	RDAAFPQIPDP KQFOPVPAISI UPSCCNVGPQ TRVAIIIVLPO GEKNSPHARE		165
Consensus	.DAAFPQIPDP KQFOPVPAISI UPSCCNVGPQ TRVAIIIVLPO GEKNSPHARE		250
HTLV-II Pol	CQPAATNEM RKMETSITIV QYMDPDLIAS PTNEEDDOES DIILQLDTIE		300
HTLV-I Pol	MQIAAHPIQIT RQADQOQML QYMDPDLIAS PSHESLIES EAMMASLISH		215
Consensus	.QPAATNEM RKMETSITIV QYMDPDLIAS PTNEEDDOES DIILQLDTIE		300
HTLV-II Pol	EEENISQEKILO QIPECEPHEC OISPNELIY CSPEHETIKS QMIIIELOVI		350
HTLV-I Pol	EEIVSSENKIQO QIPECEPHEC OISPNELIY CSPEHETIKS QMIIIELOVI		265
Consensus	EEENISQEKILO QIPECEPHEC OISPNELIY CSPEHETIKS QMIIIELOVI		350
HTLV-II Pol	EGHICQIVWSKG IVIIQKHDOSRYSRSHGYRDVPACTHIDQ OLHIAHAIQC		400
HTLV-I Pol	EGHICQIVWSKG IVIIQKHDOSRYSRSHGYRDVPACTHIDQ OVOQIVQLRC		315
Consensus	EGHICQIVWSKG IVIIQKHDOSRYSRSHGYRDVPACTHIDQ OVOQIVQLRC		400
HTLV-II Pol	AUQHNGCNPQNPASQEPFLLISSTSTSEHISV CQKOMIPQ AAWAHPHED		450
HTLV-I Pol	AUSCDNCSSTVQVIIPEVAAATMILLTEHIV VQOSKEQMPY MWDHAPTHED		365
Consensus	AUQHNGCNPQNPASQEPFLLISSTSTSEHISV CQKOMIPQ AAWAHPHED		450
HTLV-II Pol	SICPQASHIPECTTIDRQKAKVQEVOLCGS FHHNMCKGAL CIDLRNSEHP		500
HTLV-I Pol	SOCLQACQIA SAVLQDQYQHGSVCLCOT IHNINISTOTF NOQTQTSDFP		415
Consensus	SICPQASHIPECTTIDRQKAKVQEVOLCGS FHHNMCKGAL CIDLRNSEHP		500
HTLV-II Pol	SVCQTEIHPMG RICHNGSOPS GRXVIIHLP TIDDEPRIER PIVQSEVQJL		550
HTLV-I Pol	SVFQIILHSH RICKNGSOPS GRXVIIHLP TIDDEPRIER PIVQSEVQJL		465
Consensus	SVCFTEIHPMG RICHNGSOPS GRXVIIHLP TIDDEPRIER PIVQSEVQJL		550

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HTLV-II Pol		600
HTLV-I Pol		514
Consensus		600
HTLV-II Pol		650
HTLV-I Pol		564
Consensus		650
HTLV-II Pol		700
HTLV-I Pol		614
Consensus		700
HTLV-II Pol		750
HTLV-I Pol		664
Consensus		750
HTLV-II Pol		800
HTLV-I Pol		714
Consensus		800
HTLV-II Pol		850
HTLV-I Pol		764
Consensus		850
HTLV-II Pol		900
HTLV-I Pol		814
Consensus		900
HTLV-II Pol		949
HTLV-I Pol		864
Consensus		950
HTLV-II Pol		982
HTLV-I Pol		896
Consensus		983

## Untitled-14 Formatted Alignment Pol Alignment

HTLV-II Pol	HRSRPYGYTP -DTRARAGKA PRHPDPR---	RQANQH-- PVO TPPNPPT	43
HTLV-I Pol	GKKAACNLA- ----- --NTGAS--	RPA----- RDP-----	21
HIV SF2 POL	FFREDLAFPQ GKAREFSSEQ TRANSPTSRE	IWRMAGRDNNS PSEAGADRQG	50
Consensus	.....- . R..... R...P.-	.....MA..... P...P.....	50
HTLV-II Pol	HI-LALPKVP -RYPFLLPLR HPQQMDH--	----- HWKG	72
HTLV-I Pol	-----PKAP -R-----	-----	26
HIV SF2 POL	TVSFNLQQT LWQRPIVTIK IGGQLKEALL DTGADDIVLE EMNLPGRWKP	100	
Consensus	...-.L.P -R..... .Q....-	----- WK.	100
HTLV-II Pol	RPTTMPGASI PPPR-----	PQPPPPI AANSHSKHHR	102
HTLV-I Pol	-----	-----	26
HIV SF2 POL	KMIGGIGGFI KVRQYDQILI EICGHKAIGT VLVGPTPVNI IGRNLLTQLG	150	
Consensus	.....G..I ..R.-	-----P.P..I .....	150
HTLV-II Pol	PRTPSPTSP- -SGHISHKPE ---RLQ--A	ND----- S--KAES-Ac	136
HTLV-I Pol	----- -NQEPMPHKPE ---RLQ--A	QH----- R--KAES-Ac	51
HIV SF2 POL	CTLNFPISPI ETVENKLKEG MDGPKVKQWP	EEEKIKW----- EICTEMPKEC	200
Consensus	....P.SP- ...E.PKEE ---RLQ--A	.....V----- S--KAES-Ac	200
HTLV-II Pol	HIEPY-----CPGNNEVTPKK PNC-KWRFIH	DPATNAINT TLTSPSPCPP	183
HTLV-I Pol	HIEPYT-----CPGNNEVTPKK PANG-TWRFIH	DUPATNSLII DLSSSSPCPP	98
HIV SF2 POL	KISKVGOPENP YNIPVBAIKK KESTKWRKLV	DFRELINKRQ DFWEVQLCDE	250
Consensus	HIEPY.-----CPGNNEVTPKK PNC-KWRFIH	D.PATN. .... DL.S.SPCPP	250
HTLV-II Pol	DLSSTPTALP HLQTIELRDA FEQIPEPKY QRYFAEIMDQ PCNYGPEIRY	233	
HTLV-I Pol	DLSSTPTTLA HLQTIELRDA FEQIPEPKOF QRYFAEIMDQ QCNYGPEIRY	148	
HIV SF2 POL	HPCGKKKK-K SVTIVLNGCA MMSMPDKF RKYIWAQHES INNETPSIRY	299	
Consensus	DLSSTPT.L. HLQTIEL. FEQIPEPKOF QRYFAEIMDQ .CNYGPEIRY	300	
HTLV-II Pol	AWI-----ECK NSPILIE QQ-----AV NMRKM FPTSTIVCYM DDILLASPTN	283	
HTLV-I Pol	AWKVI-----ECK NSPILIE EQ-----AV CPTROA FIPQCTILQHM DDILLASPSH	198	
HIV SF2 POL	QYN-----OAK GSP-----SSV KQ-----EPRKQ NPDIVYVVA DPLYVGSDLE	349	
Consensus	AW.-----ECK NSPILIE .Q.-----E.EK. FV. .... DDILLASP..	350	
HTLV-II Pol	EELQQLSQLT QALTTTGLP ISQ-----TP GQIRF QVI SP.HIYIST	333	
HTLV-I Pol	EDLLLSEAT VASLISHGLP V-----TP GTIKF QII SP.HIYDAV	248	
HIV SF2 POL	IGQHRTKIEE TROHLLRWGF T-----PKKE PPFLW SYEL HECKWIVQPI	399	
Consensus	E.L..LS..T ...L..HGLP .....TP G.I.F Q.I SENH.AY..	400	
HTLV-II Pol	PTI-----IKSQW LTHLQVILE I-----MSKGTPi LRKHLOSTMS A-----HYRDPR	383	
HTLV-I Pol	PTV-----IRSRW LP-----ALIIE I-----MSKGTPi LRQPLHSYMC A-----QRHTDPRD	298	
HIV SF2 POL	-M-----EKDSV VNDI-----KLWVK LNA-----SQIYAG IK--VKNICK L-----RGTKALTE	446	
Consensus	PT-----IKS. ....L..L.-----LIE I-----MSKGTP. LR..L.SY. A-----G..DPR.	450	

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HTLV-II Pol	CQHITPQQQLH	AHAIQGALQ	HNCRGRGLNPA	LPLIGLISDS	TSGITTSVIF	433
HTLV-I Pol	CHMENPSVQQ	SIVQLRGALS	QNCRSRSLVQT	LPLIGAIMLT	LTGTTTVF	348
HIV SF2 Pol	VIPHTTEAEL	EIAENREIILK	EPVHGVYYDP	SKDIIVAEIQ	KOGOGQWTY	495
Consensus	.H.I.P.Q.	.E...RQA.	.NCRGRL...	LPLIG.I...	.TGT.T.V.H	500
HTLV-II Pol	PKONWPLAWG	HIPHPPPTSLC	PWGHLACTI	LTLGKMLQS	YGQLCQSFHH	483
HTLV-I Pol	SKEQWLVLWL	HAHPLPHTSQC	PWGQLLASAV	LLLGKMLQS	YGLLCQIHH	398
HIV SF2 Pol	IYOE-EFKNL	KIGKGKYARMRG	AHTNDVKQLT	EAVOKIITQS	IVIWGKIPKF	544
Consensus	.KQ.WL.W	HDP.P.TS.C	PWG.LLA...	L.LGKMLQS	YG.LCQI.HH	550
HTLV-II Pol	NMSKQALC-D	FLRNSPHPSV	GILIHJMGRF	HNGSQPSGP	WKTLLHLPTL	532
HTLV-I Pol	NISTGTFN-D	FIQTSDDHPSV	HILLHHSHRF	KNGAQTGEL	WNTFLKTAAP	447
HIV SF2 Pol	KLPICKETWE	AAWTEYWOAT	WPEWEFVNT	PHVVKLWYQL	EKDPIVGAET	594
Consensus	N.S.Q....	F..TS.HPSV	.IL.HH..RF	.NG.Q...L	WKT.L..A..	600
HTLV-II Pol	LQEPRLLLRPPI	FTLSPVVLDIT	APCLFSDGSP	QKAYVVLWQ	TILOODITPL	582
HTLV-I Pol	LAPVKALMPV	FTLSPVIINT	APCLFSDGST	SRAAYILWQK	QILSQRSFPL	497
HIV SF2 Pol	FYVDGANRE	TKIGKAGYVT	DRGRQKVSL	TDMINQKTEL	QAIHLALQDS	644
Consensus	L....AL.P.	FTLSPV...	APCLFSDG...	...AA.Y.LWD.	QIL.Q...PL	650
HTLV-II Pol	PSHETHSIACK	GELIALICGL	RAAKPWPSLN	IFLISKYLIK	YLHSLAIGNF	632
HTLV-I Pol	PPPH-KSDFR	AELGLLHGL	SSARSWRCLN	IFLISKYLYH	YLRTLALGTF	546
HIV SF2 Pol	GLEVNIVTTS	QYALGIQAO	PDKSESELVS	QIISQLIKKE	KVYLAWPAH	694
Consensus	P.....SAQ.	.EL.GLI.GL	..A..W..LN	IFLISKYL..	YL..LA.GAF	700
HTLV-II Pol	IETSAHQTLQ	AALPPPLQGK	ITVYHHVRSH	TNLPPDPISTF	NEYTLDSEILA	682
HTLV-I Pol	QERSSQAPFD	ALLPRRLSRK	VVMHHVRSH	TNLPPDPISR	NALTDAILLI	596
HIV SF2 Pol	KCIGGNEQVD	KLVSAGI-RK	VLFDG-----	DKAQEEHEKY	BSNWRAM--A	738
Consensus	.E.S.....Q	ALLP.LL.RK	V.YHHVRSH	TNLPPDPI..	N..TDAL..A	750
HTLV-II Pol	PLVP	QGL	HGLTHCNQRA	LVSFGATPRE	AKSLVO	732
HTLV-I Pol	PVLQ	SPAEI	HSFTHCGQTA	LTLQGATTTE	ASNLIR	646
HIV SF2 Pol	SDFN	-----	-----	VV-----	KEIVASDK	765
Consensus	P.....L	H..THC.Q.A	LV..GAT..E	AK.IV.SH.	Q..N.QH.M	800
HTLV-II Pol	PRGYRRGLL	PNHITNGCDM	SYKYKNTKYKC	IENWVDTFSG	AUSVSCKKK	782
HTLV-I Pol	PRGHRRGLL	PNHITNGCDI	IFKYKNTLYR	IENWVDTFSG	AISATQKRKE	696
HIV SF2 Pol	-HQGIDCS--	PG-TNGIDCT	IELEGKIIILVA	WVY-ASGY--	-HEAEVIPAD	807
Consensus	PRG.YRRGLL	PNHITNGCDI	.KYK..LY.	IENWVDTFSG	AUSA..K.KE	850
HTLV-II Pol	ISCH	ISAVD	QAISSLGKPL	HNGP	IQEFQEFGT	832
HTLV-I Pol	ISSP	ISSII	QAI AHLGKPS	YANWNGP	IQDFLNMGT	746
HIV SF2 Pol	IGQF	DAYFII	KLAGRWPVKT	TSNSF	TTTVKAAGW	856
Consensus	IS.S.IIS..	QAI..LGKP.	.NNGP	I.Q.F...GT	S...K.K.TH	900

# Untitled-14 Formatted Alignment

HTLV-II Pol	PVNPISSGLVWERTNGVIRNL LNKYLLPCPN	PPLDNAIHKA LWTLNQLNVM	882
HTLV-I Pol	PVNPISSGLVWERTNGVIRNL LNKYLLPCPN	PPLDNAIHKA LWTLNQLNVM	796
HIV SF2 P01	PVNPISSGLVWERTNGVIRNL LNKYLLPCPN	PPLDNAIHKA LWTLNQLNVM	906
Consensus	PVNPISSGLVWERTNGVIRNL LNKYLLPCPN	PPLDNAIHKA LWTLNQLNVM	950
HTLV-II Pol	NPSGKTRWQI HHSPPLPPPIP	EASTPPPKPPP KWFYYKLPGL TNQRWKGPLO	932
HTLV-I Pol	TNCHKTRWQL HHSPRLQPIP	EPRSLSNKQT HWYYFKLPGL NSRQWKGPQE	846
HIV SF2 P01	GGYSAGERIV DILATDIQTK	ELQKQITKIQ NFRVY-YRDS REPLWKGPAK	955
Consensus	....KTRWQ. HHSP.L.PIP	.....K... .W.YYKLPGL ....WKGP..	1000
HTLV-II Pol	SIQEAAAGAL LSIDGS-PRW	IPARFLIKAA CPRPDASELA EHAATDHCHH	981
HTLV-I Pol	ATQEAAAGAL IPVASSAQW	IPARLILKRAA CPRPVGGP-A DPKEKDLCHH	895
HIV SF2 P01	LIWKGECAVV IQDNSD-IKV	MPRR--KAKI IRDYGKQMAG DDCVASRODE	1002
Consensus	.IQEAAAGAL I...S...W	IPWEN..LK..AA CPRP.....A D....D.CHH	1050
HTLV-II Pol	G		982
HTLV-I Pol	G		896
HIV SF2 P01	D		1003
Consensus	G		1051

# Untitled-13 Formatted Alignment

HTLV-I/II

GAG ALIGNMENT

HTLV-II Gag		50
HTLV-I gag		50
Consensus		50
HTLV-II Gag		100
HTLV-I gag		93
Consensus		100
HTLV-II Gag		143
HTLV-I gag		137
Consensus		150
HTLV-II Gag		193
HTLV-I gag		187
Consensus		200
HTLV-II Gag		243
HTLV-I gag		237
Consensus		250
HTLV-II Gag		293
HTLV-I gag		287
Consensus		300
HTLV-II Gag		343
HTLV-I gag		337
Consensus		350
HTLV-II Gag		393
HTLV-I gag		387
Consensus		400
HTLV-II Gag		433
HTLV-I gag		429
Consensus		444

Untitled-13 Formatted Alignment

HTLV-I/II : HIV-I  
GAG ALIGNMENT

HTLV-II Gag	MQQIHG-LSP TPIPKAPRGL STHWLNFQ AAYRLQPRPS DFDFQLRRF	49
HTLV-I gag	MQQIFS-RSA SPIPRPPRGL AAHHWLNFQ AAYRLEPGPS SYDFQLKKF	49
HIV SF2 Gag	MQARASVLSG GELDKWEKIR LRPGGKKYQ LKHIVWASRE LERPAINPGL	50
Consensus	MQI.S-LSP . PIPK.PRGL .. HHWLNFQ AAYRL.P.PS .. DF.QL..F	50
HTLV-II Gag	EKLALKTPPIW LNPIPYSLA SLIPKGYPGR VVEIINILVK NQVSPSAPAA	99
HTLV-I gag	EKINLETPAR ICPINYSLLA SLLPKGYPGR VNEILHILIQ TQ-----A	92
HIV SF2 Gag	ETSEGRQI LGQLOPHSLKT GSEEIRSLYN TVATLYCVHQ KIEVKDTKEA	100
Consensus	EK..AL.TP.. L.PI.PYSLA SL.PKGYPGR VVEIL.IL.Q.Q.....A	100
HTLV-II Gag	PVPTPICPTT TPPPPPPPSP -----EAH VHEPYVEPTT TQCFPILHPP	142
HTLV-I gag	QIPSR---- -PAPPPPSSP THDPPDSDPVH EHPYVEPTA PQVLPVMHPP	136
HIV SF2 Gag	LDKIEEEQNQ SKKKAQQTAA DTGNSSQVSO NYPTIVONLQG QMVHQPISPR	150
Consensus	.P..... .P.PPPP.SP ..... Q.HEPYVEPT. .QV.P..HP.	150
HTLV-II Gag	GAPSAHRPWO MKDL-QAIIKQ EVSSA...G-S POFMOTIRLA VQQFDPTIAKD	190
HTLV-I gag	GAPPNHRPWO MKDL-QAIIKQ EVSQAA...G-S POFMOTIRLA VQQFDPTIAKD	184
HIV SF2 Gag	TLNAWKVVE EKAFAFSPEVTP MEFALAEQSAT POFDENIMLNTP VGGHOAAMQM	200
Consensus	GAP..HRPWO MKDL-QAIIKQ EVS...A.G-S POFMOTIRLA VQQFDPTIAKD	200
HTLV-II Gag	QDLQYLCS SL--VVSLHH QOLN-TLITE AETRGMIIGYN PMAGPLRMOA	237
HTLV-I gag	QDLQYLCS SL--VASLHH QQLD-SLISE AETRGMIIGYN PLAGPLRVQA	231
HIV SF2 Gag	EKETINEEEAA EWDRRLHPVHA GPIAPGQMRE PRGSDIAGIT STLQEIQIGWM	250
Consensus	QDLQYLCS SL--V.SLHH QQL.-.LI.E AETRGMIIGYN P.AGPLR.QA	250
HTLV-II Gag	NPAQQQLRR EYQNLWLAAF STLPGNTRDP SWAATI...GEL EPIYCAFVERL	287
HTLV-I gag	NPQQQQQLRR EYQQLWLAAF YALPGSAKDP SWASHI...GEL EPIYCAFVERL	281
HIV SF2 Gag	TNPPIPVG EYKRWIILGL NKIVRMYSPY TILDIFOSPK EYFRDYVYRFT	300
Consensus	N.P.QQQLRR EYQ.LWLAAF .LPG...DP SWA...GEL EPIYCAFVERL	300
HTLV-II Gag	NVTDGLPE GTHK PILRS DAVSNANKCQ KQIKICRSHI NSHEGYVRA	337
HTLV-I gag	NVTDGLPE GTHK PILRS DAVSNANKCQ KQIKICRSHI NSHEGYVRA	331
HIV SF2 Gag	YKIDRREQAS QDVKWMTE DLVONANPDC KTIDKALEPVA GTFEEMTA	349
Consensus	N.VTDGLPE GTHK PILRS DAVSNANKCQ KQIKICRSHI NSHEGYVRA	350
HTLV-II Gag	AW-TPKDKI UKV----- VVQP ---RRPPPTQ PGCGCKVGH	371
HTLV-I gag	TW-TPKDKI UKV----- VVQP ---KKPPPNQ PGCGCKKACH	365
HIV SF2 Gag	GVGGEGHK RFRV AEAMSQ VNSVTVMMSK GNFKNQRKTV KGCGCKECH	399
Consensus	.W-TPKDKI UKV----- VVQP ---K.PPPTQ PGCGCKKACH	400
HTLV-II Gag	WSRGTGTPR PPG-H----- PI COGP ----- SHI KRDP --Q	401
HTLV-I gag	WSRGTGTPR PPG-H----- PI COGP ----- THI KRDP --R	395
HIV SF2 Gag	IAKNGRAPRK KGCWKGGREG HONKIDT2RQ ANFLGKIPPS HKGRPGNFLQ	449
Consensus	WSRGTGTPR PPG-H----- PI COGP ----- .HI KRDP --Q	450

### Untitled-13 Formatted Alignment

HTLV-II Gag	LKE-----RQE[E]-----G[Q]-----PLLLD[L]ST SG---TTEEK N[SLRG]EI---	433
HTLV-I gag	LKE[TIPE]P[E]-----E[D]-----A[L]L[L]D[L] AD---IPH PK N[FIGGEV]---	429
HIV SF2 Gag	N[R]EPTAPP[A] S[F]GFG[G]ETT TPPQ[KOH]RID KGLYPLTS LR SLFGN[D]PSSQ	499
Consensus	LKE.....[E]...[E]-----G[Q]-----PLLLD[L]P...G---.T..K N..GGE.---	500